OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/081,806

DATE: 07/02/2002
TIME: 14:00:32

Input Set : N:\Crf3\RULE60\10081806.raw
Output Set: N:\CRF3\07022002\J081806.raw

SEQUENCE LISTING

```
  3 (1) GENERAL INFORMATION:
  5      (i) APPLICANT: Prudent, James R.
  6                    Hall, Jeff G.
  7                    Lyamichev, Victor I.
  9     (ii) TITLE OF INVENTION: Invasive Cleavge Of Nucleic Acids
 11    (iii) NUMBER OF SEQUENCES: 69
 13     (iv) CORRESPONDENCE ADDRESS:
 14          (A) ADDRESSEE: Medlen & Carroll, LLP
 15          (B) STREET: 220 Montgomery Street, Suite 2200
 16          (C) CITY: San Francisco
 17          (D) STATE: California
 18          (E) COUNTRY: United States Of America
 19          (F) ZIP: 94104
 21      (v) COMPUTER READABLE FORM:
 22          (A) MEDIUM TYPE: Floppy disk
 23          (B) COMPUTER: IBM PC compatible
 24          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 25          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 27     (vi) CURRENT APPLICATION DATA:
 28          (A) APPLICATION NUMBER: US/10/081,806       C-->
 29          (B) FILING DATE: 22-Feb-2002                C-->
 30          (C) CLASSIFICATION:
 40    (vii) PRIOR APPLICATION DATA:
 33          (A) APPLICATION NUMBER: US/08/756,386
 34          (B) FILING DATE:
 37          (A) APPLICATION NUMBER: US 08/682,853
 38          (B) FILING DATE: 12-JUL-1996
 41          (A) APPLICATION NUMBER: US 08/599,491
 42          (B) FILING DATE: 24-JAN-1996
 44   (viii) ATTORNEY/AGENT INFORMATION:
 45          (A) NAME: Ingolia, Diane E.
 46          (B) REGISTRATION NUMBER: 40,027
 47          (C) REFERENCE/DOCKET NUMBER: FORS-02564
 49     (ix) TELECOMMUNICATION INFORMATION:
 50          (A) TELEPHONE: (415) 705-8410
 51          (B) TELEFAX: (415) 397-8338
 54 (2) INFORMATION FOR SEQ ID NO: 1:
 56      (i) SEQUENCE CHARACTERISTICS:
 57          (A) LENGTH: 2506 base pairs
 58          (B) TYPE: nucleic acid
 59          (C) STRANDEDNESS: double
 60          (D) TOPOLOGY: linear
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ENTERED

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62      (ii) MOLECULE TYPE: DNA (genomic)
66      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
68  ATGAGGGGGA TGCTGCCCCT CTTTGAGCCC AAGGGCCGGG TCCTCCTGGT GGACGGCCAC        60
70  CACCTGGCCT ACCGCACCTT CCACGCCCTG AAGGGCCTCA CCACCAGCCG GGGGGAGCCG       120
72  GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTCAAGGA GGACGGGGAC       180
74  GCGGTGATCG TGGTCTTTGA CGCCAAGGCC CCCTCCTTCC GCCACGAGGC CTACGGGGGG       240
76  TACAAGGCGG GCCGGGCCCC CACGCCGGAG GACTTTCCCC GGCAACTCGC CCTCATCAAG       300
78  GAGCTGGTGG ACCTCCTGGG GCTGGCGCGC CTCGAGGTCC CGGGCTACGA GGCGGACGAC       360
80  GTCCTGGCCA GCCTGGCCAA GAAGGCGGAA AAGGAGGGCT ACGAGGTCCG CATCCTCACC       420
82  GCCGACAAAG ACCTTTACCA GCTCCTTTCC GACCGCATCC ACGTCCTCCA CCCCGAGGGG       480
84  TACCTCATCA CCCCGGCCTG GCTTTGGGAA AAGTACGGCC TGAGGCCCGA CCAGTGGGCC       540
86  GACTACCGGG CCCTGACCGG GGACGAGTCC GACAACCTTC CCGGGGTCAA GGGCATCGGG       600
88  GAGAAGACGG CGAGGAAGCT TCTGGAGGAG TGGGGGGAGCC TGGAAGCCCT CCTCAAGAAC       660
90  CTGGACCGGC TGAAGCCCGC CATCCGGGAG AAGATCCTGG CCCACATGGA CGATCTGAAG       720
92  CTCTCCTGGG ACCTGGCCAA GGTGCGCACC GACCTGCCCC TGGAGGTGGA CTTCGCCAAA       780
94  AGGCGGGAGC CCGACCGGGA GAGGCTTAGG GCCTTTCTGG AGAGGCTTGA GTTTGGCAGC       840
96  CTCCTCCACG AGTTCGGCCT TCTGGAAAGC CCCAAGGCCC TGGAGGAGGC CCCCTGGCCC       900
98  CCGCCGGAAG GGGCCTTCGT GGGCTTTGTG CTTTCCCGCA AGGAGCCCAT GTGGGCCGAT       960
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104 CTGAGGGAAG GCCTTGGCCT CCCGCCCGGC GACGACCCCA TGCTCCTCGC CTACCTCCTG      1140
106 GACCCTTCCA ACACCACCCC CGAGGGGGTG GCCCGGCGCT ACGGCGGGGA GTGGACGGAG      1200
108 GAGGCGGGGG AGCGGGCCGC CCTTTCCGAG AGGCTCTTCG CCAACCTGTG GGGGAGGCTT      1260
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114 CTGGAGGTGG CCGAGGAGAT CGCCCGCCTC GAGGCCGAGG TCTTCCGCCT GGCCGGCCAC      1440
116 CCCTTCAACC TCAACTCCCG GGACCAGCTG GAAAGGGTCC TCTTTGACGA GCTAGGGCTT      1500
118 CCCGCCATCG GCAAGACGGA GAAGACCGGC AAGCGCTCCA CCAGCGCCGC CGTCCTGGAG      1560
120 GCCCTCCGCG AGGCCCACCC CATCGTGGAG AAGATCCTGC AGTACCGGGA GCTCACCAAG      1620
122 CTGAAGAGCA CCTACATTGA CCCCTTGCCG GACCTCATCC ACCCCAGGAC GGGCCGCCTC      1680
124 CACACCCGCT TCAACCAGAC GGCCACGGCC ACGGGCAGGC TAAGTAGCTC CGATCCCAAC      1740
126 CTCCAGAACA TCCCCGTCCG CACCCCGCTT GGGCAGAGGA TCCGCCGGGC CTTCATCGCC      1800
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130 CACCTCTCCG GCGACGAGAA CCTGATCCGG GTCTTCCAGG AGGGGCGGGA CATCCACACG      1920
132 GAGACCGCCA GCTGGATGTT CGGCGTCCCC CGGGAGGCCG TGGACCCCCT GATGCGCCGG      1980
134 GCGGCCAAGA CCATCAACTT CGGGGTCCTC TACGGCATGT CGGCCCACCG CCTCTCCCAG      2040
136 GAGCTAGCCA TCCCTTACGA GGAGGCCCAG GCCTTCATTG AGCGCTACTT TCAGAGCTTC      2100
138 CCCAAGGTGC GGGCCTGGAT TGAGAAGACC CTGGAGGAGG CAGGAGGCG GGGGTACGTG       2160
140 GAGACCCTCT TCGGCCGCCG CCGCTACGTG CCAGACCTAG AGGCCCGGGT GAAGAGCGTG      2220
142 CGGGAGGCGG CCGAGCGCAT GGCCTTCAAC ATGCCCGTCC AGGGCACCGC CGCCGACCTC      2280
144 ATGAAGCTGG CTATGGTGAA GCTCTTCCCC AGGCTGGAGG AAATGGGGGC CAGGATGCTC      2340
146 CTTCAGGTCC ACGACGAGCT GGTCCTCGAG GCCCCAAAAG AGAGGGCGGA GGCCGTGGCC      2400
148 CGGCTGGCCA AGGAGGTCAT GGAGGGGGTG TATCCCCTGG CCGTGCCCCT GGAGGTGGAG      2460
150 GTGGGGATAG GGGAGGACTG GCTCTCCGCC AAGGAGTGAT ACCACC                    2506
152 (2) INFORMATION FOR SEQ ID NO: 2:
154      (i) SEQUENCE CHARACTERISTICS:
155          (A) LENGTH: 2496 base pairs
156          (B) TYPE: nucleic acid
157          (C) STRANDEDNESS: double
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158          (D) TOPOLOGY: linear
160     (ii) MOLECULE TYPE: DNA (genomic)
164     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
166 ATGGCGATGC TTCCCCTCTT TGAGCCCAAA GGCCGCGTGC TCCTGGTGGA CGGCCACCAC     60
168 CTGGCCTACC GCACCTTCTT TGCCCTCAAG GGCCTCACCA CCAGCCGCGG CGAACCCGTT    120
170 CAGGCGGTCT ACGGCTTCGC CAAAAGCCTC CTCAAGGCCC TGAAGGAGGA CGGGGACGTG    180
172 GTGGTGGTGG TCTTTGACGC CAAGGCCCCC TCCTTCCGCC ACGAGGCCTA CGAGGCCTAC    240
174 AAGGCGGGCC GGGCCCCCAC CCCGGAGGAC TTTCCCCGGC AGCTGGCCCT CATCAAGGAG    300
176 TTGGTGGACC TCCTAGGCCT TGTGCGGCTG GAGGTTCCCG GCTTTGAGGC GGACGACGTG    360
178 CTGGCCACCC TGGCCAAGCG GGCGGAAAAG GAGGGGTACG AGGTGCGCAT CCTCACTGCC    420
180 GACCGCGACC TCTACCAGCT CCTTTCGGAG CGCATCGCCA TCCTCCACCC TGAGGGGTAC    480
182 CTGATCACCC CGGCGTGGCT TTACGAGAAG TACGGCCTGC GCCCGGAGCA GTGGGTGGAC    540
184 TACCGGGCCC TGGCGGGGGA CCCCTCGGAT AACATCCCCG GGGTGAAGGG CATCGGGGAG    600
186 AAGACCGCCC AGAGGCTCAT CCGCGAGTGG GGGAGCCTGG AAAACCTCTT CCAGCACCTG    660
188 GACCAGGTGA AGCCCTCCTT GCGGGAGAAG CTCCAGGCGG GCATGGAGGC CCTGGCCCTT    720
190 TCCCGGAAGC TTTCCCAGGT GCACACTGAC CTGCCCCTGG AGGTGGACTT CGGGAGGCGC    780
192 CGCACACCCA ACCTGGAGGG TCTGCGGGCT TTTTTGGAGC GGTTGGAGTT TGGAAGCCTC    840
194 CTCCACGAGT TCGGCCTCCT GGAGGGGCCG AAGGCGGCAG AGGAGGCCCC CTGGCCCCCT    900
196 CCGGAAGGGG CTTTTTTGGG CTTTTCCTTT TCCCGTCCCG AGCCCATGTG GGCCGAGCTT    960
198 CTGGCCCTGG CTGGGGCGTG GGAGGGGCGC CTCCATCGGG CACAAGACCC CCTTAGGGGC   1020
200 CTGAGGGACC TTAAGGGGGT GCGGGGAATC CTGGCCAAGG ACCTGGCGGT TTTGGCCCTG   1080
202 CGGGAGGGCC TGGACCTCTT CCCAGAGGAC GACCCCATGC TCCTGGCCTA CCTTCTGGAC   1140
204 CCCTCCAACA CCACCCCTGA GGGGGTGGCC CGGCGTTACG GGGGGGAGTG GACGGAGGAT   1200
206 GCGGGGGAGA GGGCCCTCCT GGCCGAGCGC CTCTTCCAGA CCCTAAAGGA GCGCCTTAAG   1260
208 GGAGAAGAAC GCCTGCTTTG GCTTTACGAG GAGGTGGAGA AGCCGCTTTC CCGGGTGTTG   1320
210 GCCCGGATGG AGGCCACGGG GGTCCGGCTG GACGTGGCCT ACCTCCAGGC CCTCTCCCTG   1380
212 GAGGTGGAGG CGGAGGTGCG CCAGCTGGAG GAGGAGGTCT TCCGCCTGGC CGGCCACCCC   1440
214 TTCAACCTCA ACTCCCGCGA CCAGCTGGAG CGGGTGCTCT TTGACGAGCT GGGCCTGCCT   1500
216 GCCATCGGCA AGACGGAGAA GACGGGGAAA CGCTCCACCA GCGCTGCCGT GCTGGAGGCC   1560
218 CTGCGAGAGG CCCACCCCAT CGTGGACCGC ATCCTGCAGT ACCGGGAGCT CACCAAGCTC   1620
220 AAGAACACCT ACATAGACCC CCTGCCCGCC CTGGTCCACC CCAAGACCGG CCGGCTCCAC   1680
222 ACCCGCTTCA ACCAGACGGC CACCGCCACG GGCAGGCTTT CCAGCTCCGA CCCCAACCTG   1740
224 CAGAACATCC CCGTGCGCAC CCCTCTGGGC CAGCGCATCC GCCGAGCCTT CGTGGCCGAG   1800
226 GAGGGCTGGG TGCTGGTGGT CTTGGACTAC AGCCAGATTG AGCTTCGGGT CCTGGCCCAC   1860
228 CTCTCCGGGG ACGAGAACCT GATCCGGGTC TTTCAGGAGG GGAGGGACAT CCACACCCAG   1920
230 ACCGCCAGCT GGATGTTCGG CGTTTCCCCC GAAGGGGTAG ACCCTCTGAT GCGCCGGGCG   1980
232 GCCAAGACCA TCAACTTCGG GGTGCTCTAC GGCATGTCCG CCCACCGCCT CTCCGGGGAG   2040
234 CTTTCCATCC CCTACGAGGA GGCGGTGGCC TTCATTGAGC GCTACTTCCA GAGCTACCCC   2100
236 AAGGTGCGGG CCTGGATTGA GGGGACCCTC GAGGAGGGCC GCCGGCGGGG GTATGTGGAG   2160
238 ACCCTCTTCG GCCGCCGGCG CTATGTGCCC GACCTCAACG CCCGGGTGAA GAGCGTGCGC   2220
240 GAGGCGGCGG AGCGCATGGC CTTCAACATG CCGGTCCAGG GCACCGCCGC CGACCTCATG   2280
242 AAGCTGGCCA TGGTGCGGCT TTTCCCCCGG CTTCAGGAAC TGGGGGCGAG GATGCTTTTG   2340
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248 GGCCTGGGGG AGGACTGGCT CTCCGCCAAG GAGTAG                            2496
250 (2) INFORMATION FOR SEQ ID NO: 3:
252     (i) SEQUENCE CHARACTERISTICS:
253          (A) LENGTH: 2504 base pairs
254          (B) TYPE: nucleic acid
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Output Set: N:\CRF3\07022002\J081806.raw

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255          (C) STRANDEDNESS: double
256          (D) TOPOLOGY: linear
258     (ii) MOLECULE TYPE: DNA (genomic)
262     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
264 ATGGAGGCGA TGCTTCCGCT CTTTGAACCC AAAGGCCGGG TCCTCCTGGT GGACGGCCAC        60
266 CACCTGGCCT ACCGCACCTT CTTCGCCCTG AAGGGCCTCA CCACGAGCCG GGGCGAACCG       120
268 GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTGAAGGA GGACGGGTAC       180
270 AAGGCCGTCT TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGAG       240
272 GCCTACAAGG CGGGGAGGGC CCCGACCCCC GAGGACTTCC CCCGGCAGCT CGCCCTCATC       300
274 AAGGAGCTGG TGGACCTCCT GGGGTTTACC CGCCTCGAGG TCCCCGGCTA CGAGGCGGAC       360
276 GACGTTCTCG CCACCCTGGC CAAGAAGGCG GAAAAGGAGG GGTACGAGGT GCGCATCCTC       420
278 ACCGCCGACC GCGACCTCTA CCAACTCGTC TCCGACCGCG TCGCCGTCCT CCACCCCGAG       480
280 GGCCACCTCA TCACCCCGGA GTGGCTTTGG GAGAAGTACG GCCTCAGGCC GGAGCAGTGG       540
282 GTGGACTTCC GCGCCCTCGT GGGGGACCCC TCCGACAACC TCCCCGGGGT CAAGGGCATC       600
284 GGGGAGAAGA CCGCCCTCAA GCTCCTCAAG GAGTGGGGAA GCCTGGAAAA CCTCCTCAAG       660
286 AACCTGGACC GGGTAAAGCC AGAAAACGTC CGGGAGAAGA TCAAGGCCCA CCTGGAAGAC       720
288 CTCAGGCTCT CCTTGGAGCT CTCCCGGGTG CGCACCGACC TCCCCCTGGA GGTGGACCTC       780
290 GCCCAGGGGC GGGAGCCCGA CCGGGAGGGG CTTAGGGCCT TCCTGGAGAG GCTGGAGTTC       840
292 GGCAGCCTCC TCCACGAGTT CGGCCTCCTG GAGGCCCCCG CCCCCCTGGA GGAGGCCCCC       900
294 TGGCCCCCGC CGGAAGGGGC CTTCGTGGGC TTCGTCCTCT CCCGCCCCGA GCCCATGTGG       960
296 GCGGAGCTTA AAGCCCTGGC CGCCTGCAGG GACGGCCGGG TGCACCGGGC AGCAGACCCC      1020
298 TTGGCGGGGC TAAAGGACCT CAAGGAGGTC CGGGGCCTCC TCGCCAAGGA CCTCGCCGTC      1080
300 TTGGCCTCGA GGGAGGGGCT AGACCTCGTG CCCGGGGACG ACCCCATGCT CCTCGCCTAC      1140
302 CTCCTGGACC CCTCCAACAC CACCCCCGAG GGGGTGGCGC GGCGCTACGG GGGGGAGTGG      1200
304 ACGGAGGACG CCGCCCACCG GGCCCTCCTC TCGGAGAGGC TCCATCGGAA CCTCCTTAAG      1260
306 CGCCTCGAGG GGGAGGAGAA GCTCCTTTGG CTCTACCACG AGGTGGAAAA GCCCCTCTCC      1320
308 CGGGTCCTGG CCCACATGGA GGCCACCGGG GTACGGCTGG ACGTGGCCTA CCTTCAGGCC      1380
310 CTTTCCCTGG AGCTTGCGGA GGAGATCCGC CGCCTCGAGG AGGAGGTCTT CCGCTTGGCG      1440
312 GGCCACCCCT TCAACCTCAA CTCCCGGGAC CAGCTGGAAA GGGTGCTCTT TGACGAGCTT      1500
314 AGGCTTCCCG CCTTGGGGAA GACGCAAAAG ACAGGCAAGC GCTCCACCAG CGCCGCGGTG      1560
316 CTGGAGGCCC TACGGGAGGC CCACCCCATC GTGGAGAAGA TCCTCCAGCA CCGGGAGCTC      1620
318 ACCAAGCTCA AGAACACCTA CGTGGACCCC CTCCCAAGCC TCGTCCACCC GAGGACGGGC      1680
320 CGCCTCCACA CCCGCTTCAA CCAGACGGCC ACGGCCACGG GGAGGCTTAG TAGCTCCGAC      1740
322 CCCAACCTGC AGAACATCCC CGTCCGCACC CCCTTGGGCC AGAGGATCCG CCGGGCCTTC      1800
324 GTGGCCGAGG CGGGTTGGGC GTTGGTGGCC CTGGACTATA GCCAGATAGA GCTCCGCGTC      1860
326 CTCGCCCACC TCTCCGGGGA CGAAAACCTG ATCAGGGTCT TCCAGGAGGG GAAGGACATC      1920
328 CACACCCAGA CCGCAAGCTG GATGTTCGGC GTCCCCCCGG AGGCCGTGGA CCCCCTGATG      1980
330 CGCCGGGCGG CCAAGACGGT GAACTTCGGC GTCCTCTACG GCATGTCCGC CCATAGGCTC      2040
332 TCCCAGGAGC TTGCCATCCC CTACGAGGAG GCGGTGGCCT TTATAGAGGC TACTTCCAAA      2100
334 GCTTCCCCAA GGTGCGGGCC TGGATAGAAA AGACCCTGGA GGAGGGGAGG AAGCGGGGCT      2160
336 ACGTGGAAAC CCTCTTCGGA AGAAGGCGCT ACGTGCCCGA CCTCAACGCC CGGGTGAAGA      2220
338 GCGTCAGGGA GGCCGCGGAG CGCATGGCCT TCAACATGCC CGTCCAGGGC ACCGCCGCCG      2280
340 ACCTCATGAA GCTCGCCATG GTGAAGCTCT TCCCCCGCCT CCGGGAGATG GGGGCCCGCA      2340
342 TGCTCCTCCA GGTCCACGAC GAGCTCCTCC TGGAGGCCCC CCAAGCGCGG GCCGAGGAGG      2400
344 TGGCGGCTTT GGCCAAGGAG GCCATGGAGA AGGCCTATCC CCTCGCCGTG CCCCTGGAGG      2460
346 TGGAGGTGGG GATGGGGGAG GACTGGCTTT CCGCCAAGGG TTAG                       2504
348 (2) INFORMATION FOR SEQ ID NO: 4:
350     (i) SEQUENCE CHARACTERISTICS:
351          (A) LENGTH: 832 amino acids
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Output Set: N:\CRF3\07022002\J081806.raw

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352          (B)  TYPE: amino acid
353          (C)  STRANDEDNESS: single
354          (D)  TOPOLOGY: linear
356     (ii) MOLECULE TYPE: protein
360     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
362     Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu
363     1               5                   10                  15
365     Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly
366             20                  25                  30
368     Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
369             35                  40                  45
371     Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val
372         50                  55                  60
374     Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly
375     65                  70                  75                  80
377     Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu
378                 85                  90                  95
380     Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu
381                 100                 105                 110
383     Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys
384                 115                 120                 125
386     Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp
387             130                 135                 140
389     Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly
390     145                 150                 155                 160
392     Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro
393                 165                 170                 175
395     Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn
396                 180                 185                 190
398     Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu
399             195                 200                 205
401     Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu
402         210                 215                 220
404     Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys
405     225                 230                 235                 240
407     Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val
408                 245                 250                 255
410     Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe
411                 260                 265                 270
413     Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
414             275                 280                 285
416     Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
417         290                 295                 300
419     Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp
420     305                 310                 315                 320
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423             325                 330                 335
425     Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu
426             340                 345                 350
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/02/2002
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Input Set : N:\Crf3\RULE60\10081806.raw
Output Set: N:\CRF3\07022002\J081806.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; N Pos. 4,5,181,182,190,366,617,628,685,714,722,738,784,1022,1029
Seq#:7; N Pos. 1038,1053,1098,1105,1206,1227,1244,1251,1252,1253,1350,1380
Seq#:7; N Pos. 1497,1530,1569,1572,1641,1653,1655,1770,1812,2319,2346,2396
Seq#:8; Xaa Pos.2,63,109,186,205,209,227,228,233,240,243,244,247,260,290
Seq#:8; Xaa Pos.329,336,340,368,414,417,418,431,551,605,773,794,798,823,833
Seq#:57; N Pos. 18

VERIFICATION SUMMARY   DATE: 07/02/2002
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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:974 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:983 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:48
L:992 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:96
L:1007 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:176
L:1010 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:192
L:1013 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:208
L:1016 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:224
L:1019 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:240
L:1022 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:256
L:1028 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:288
L:1034 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:320
L:1037 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:336
L:1040 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:352
L:1049 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:400
L:1052 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:416
L:1076 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:544
L:1085 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:592
L:1118 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:768
L:1121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:784
L:1127 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:816
L:1130 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:832
L:2269 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=56
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